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Extracting Structural and Functional Features of Widely Distributed Biological Circuits with Single Cell Resolution via Tissue Clearing and Delivery Vectors

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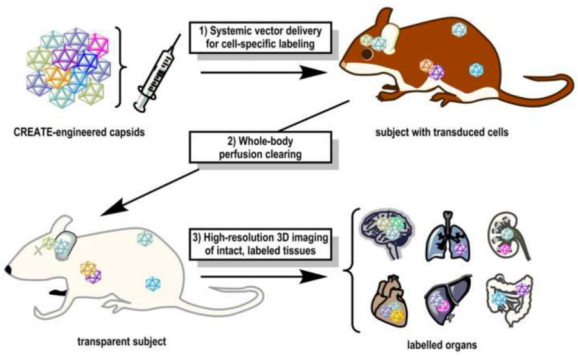
Abstract

The scientific community has learned a great deal from imaging small and naturally transparent organisms such as nematodes and zebrafish. The consequences of genetic mutations on their organ development and survival can be visualized easily and with high-throughput at the organism-wide scale. In contrast, three-dimensional information is less accessible in mammalian subjects because the heterogeneity of light-scattering tissue elements renders their organs opaque. Likewise, genetically labeling desired circuits across mammalian bodies is prohibitively slow and costly via the transgenic route. Emerging breakthroughs in viral vector engineering, genome editing tools, and tissue clearing can render larger opaque organisms genetically tractable and transparent for whole-organ cell phenotyping, tract tracing and imaging at depth.

Graphical Abstract



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Competing Interests Statement

California Institute of Technology filed intellectual property for the technologies described with authors as inventors.

Introduction – The case for a hermeneutic approach to biological investigation

From slime mold to the rhesus macaque, countless species have contributed to our current understanding of the biological processes that grant life. The optimum animal model for a line of research is often determined by a particular anatomical feature that makes the organism uniquely suitable for experimentation. For example, although the giant squid may seem an unusual choice to further understanding of mammalian neural circuits, the sheer size and slow conduction velocity of its axons enabled scientists to study neuronal firing with the rudimentary electrophysiological techniques available during the early 20th century [1], giving rise to the field of modern cellular neuroscience. By examining individual aspects of a diverse range of organisms in great detail, scientists have been able to amass a set of unifying principles for the field of neural sciences [2]. The route to this understanding parallels the hermeneutic circle, a classic concept in theology and logic [3]. In hermeneutics, the process of interpretation follows a spiraling path in which one first studies the overall body, then examines its composite parts, and lastly revisits the concept of the whole body as a sum of the parts. Similarly, in neuroscience, observation of a particular sensory or motor system in an organism leads to investigation of the cellular underpinnings of the related circuits, which are then placed in the larger context of the central and peripheral nervous systems.

Applying this approach to investigations of molecular and cellular physiology in health and disease (Table 1, first column) can be both technologically challenging and time-consuming in mammalian subjects. Mammalian tissues can be easily photographed at the macroscopic level, and then the organs and tissues can be dissected and thinly sliced for microscopic analysis. However, the process of aligning these two different perspectives to reconstruct a whole-organism map with subcellular resolution remains nontrivial [4]. Without a clear methodology for integrating microscale and macroscale views, it is difficult to apply newly-discovered molecular mechanisms to systems-level questions and to recognize how systems-level findings may in turn inform novel hypotheses on molecular processes.

Two recent technical advances can bridge the divide between cellular and systems-level studies (Table 1). First, improved viral-vector-based strategies can deliver cargo, such as fluorescent labels, efficiently and with cell specificity over entire organs or the whole body. This enables tracing of, for example, wide-coverage brain networks or peripheral nerves ([5–14], reviews: [15–20]). Second, optimized tissue-clearing methodologies (Table 2–3) can map intact local and long-range circuits [21–41]. The former merges two powerful biological techniques: the use of genetically encoded tools for studying cellular function and connectivity, and the development of viral vectors as a vehicle for delivering these tools into cells [10,11,13,19,42–54]. The latter illustrates how the century-old technique [55,56] of tissue clearing may gain renewed importance when it is refined to incorporate current advances in microscopy [27,29,57–61], genetically encoded fluorescent labeling tools [7,8,14,62–66], protein affinity tags [67–71], and tissue-binding size-adjustable polymeric scaffolding [22,29,32,37,41,72,73]. This brief review will highlight recent work on generating adeno-associated viruses with unique properties via specialized viral-vector

screening methods [53,74–80] (Figure 1, Box 1), and on modern tissue-clearing methodologies that preserve fluorescence and support high-resolution imaging at depth (Figure 2, Table 2, and Box 1; the following protocols generally achieve both goals: [21–25,28,29,31,32,35–37,39–41,81–83] and uDISCO, which outperforms 3DISCO in fluorescence preservation, personal communication with Dr. Ali Ertürk).

Scientific motivation for broad coverage gene delivery and imaging of whole intact tissues in mammals by tissue clearing

Although viral vectors are commonly used for delivering genetically encoded cargo to mammalian cells *in vivo*, therefore avoiding slow and costly transgenic means, few are capable of both safe and efficient transduction of specific cellular targets. Fewer still are capable of broad coverage across all cellular connectivity under study. For example, adeno-associated viruses (AAVs) are widely used, especially in non-dividing cells, due to their safety [78,84–86]; however, the handful of serotypes available cannot efficiently and specifically target many populations of interest. Past and ongoing efforts on engineering viral vectors with desired properties [79,87,88], including cell-type and/or organ specificity [74–77,79,89], will greatly benefit research in mapping and genome editing [90]. To contribute to and complement these efforts we have recently developed an *in vivo C*re-*RE*combination-based *A*AV *T*argeted *E*volution (CREATE) selection platform for identifying AAVs that more efficiently transduce genetically defined cell populations (Figure 1A) [53]. We used CREATE to identify variants from a systemically delivered AAV capsid library that cross the blood–brain barrier and transduce neurons and astrocytes brain-wide. Using this method, we identified one variant, AAV-PHP.B[1], that achieves 40- to 90-fold more efficient brain-wide transduction than the current standard, AAV9 (Figure 1D) [91]. AAV-PHP.B transduces most neuronal types and glia throughout the brain, which supports its use to deliver multicolor labels to genetically defined circuits for mapping distributed networks, such as those recruited by deep brain stimulation [92–97]. Furthermore, engineered vectors that label discrete cell populations could be put to immediate use, for example in elucidating points of contact between major somatic sensory nerves and the CNS, or in mapping the autonomic motor branch of the PNS to better understand metabolic and endocrine disorders.

Despite these new labeling technologies, it remains difficult to create maps for phenotypically distinct fine axons that run in bundles throughout the brain when the traditional method involves sectioning the tissue into paper-thin slices, imaging each slice, and recovering the 3D perspective with imaging software: it is slow, tedious, costly, and error prone. Over the past decade there has been a surge in methods for increasing the transparency of thick mammalian tissue samples and whole organs so that they may be examined intact (Table 2). Here, the scientific value of fluorescence-preserving tissue clearing for vector engineering is also apparent: the ability to process major organs simultaneously and without sectioning (Figure 1B–C) will greatly facilitate transduction

[1]Novel AAV capsid: AAV-PHP.B was named in honor of Caltech Professor Paul H. Patterson (1943–2014).

mapping of systemically delivered genes (Figure 1D), including small-molecule tags and fluorescent labels.

Whole-organ and whole-body tissue-clearing methodologies

The original century-old tissue-clearing techniques [55,56] enable deep imaging into tissue without physical sectioning, but the harsh organic solvents damage cellular architecture and are incompatible with modern immunolabeling and fluorescence microscopy tools. Thus, the application of modern labeling technologies to *ex vivo* mapping studies requires new developments to render tissues transparent while also stabilizing critical macromolecules and preserving endogenous fluorescence (see Table 2 for a comprehensive list of major clearing protocols of the last decade). In particular, the CLARITY technique provides a method to further stabilize samples by anchoring tissue components in place using an interpolating hydrogel scaffold [22,37]. This transparent, tissue-binding hydrogel mesh secures proteins and nucleic acids into place without causing epitope masking and allows scientists to visualize intact organs at the subcellular [40,41] and even single transcript scale [22,29,32,37,41]. Recently, a method to clear whole adult rodents and organs emerged from the realization that hydrogel monomers as well as clearing detergents and immunolabeling reagents could all be infused throughout the intact post-mortem organism using the intrinsic circulatory system (vasculature) (Figure 1B–C, Figure 2A–B) [32,41]; PARS (Perfusion-assisted Agent Release in Situ) achieves delipidation and labeling steps rapidly in the intact post-mortem organism via perfusion. The PARS approach, which has also proven compatible with a variety of tissue-clearing reagents [25,31,39,40], can prepare transparent whole organisms for imaging at depth and aligns with a paradigm shift in biomedical research. Namely, efforts to profile the two-dimensional molecular content of samples have been superseded by more comprehensive inquiries into the relationship between an organ's volumetric composition and its resulting biological function [98].

Across most disciplines and within a variety of laboratory settings, it has become increasingly relevant to engage in the fine-scale phenotyping of whole specimens, whether of intact samples, such as tissue biopsies, excised organs and cultured organs in a dish [99,100], or of whole organisms. Thus, tissue clearing methods must be simple, economical and adaptable to a variety of applications to be adopted across scientific fields. Toward this goal, we developed a set of hydrogel-embedding and delipidation protocols that can be used to rapidly clear excised organs individually or all organs simultaneously within the intact body without compromising cellular architecture or endogenous fluorescence (for experimental timeline and details, see Tables 2–3; for troubleshooting advice, see: http://www.nature.com/nprot/journal/v10/n11/fig_tab/nprot.2015.122_T5.html) [32,41]. PACT (PAssive CLARITY Technique) and PARS entail hybridizing the tissue sample to polymers in order to anchor proteins and nucleic acids during detergent-mediated lipid extraction and to preserve gross tissue architecture during all tissue-processing steps (Figure 1B–C, Figure 2A–B) [32,41]. While many clearing protocols are successful at removing lipids through detergent treatment alone, we have found that the porous structure of the tissue–hydrogel matrix, particularly when coupled to the driving force of detergent perfusion, facilitates rapid diffusion of solubilized lipids out of the tissue and the subsequent penetration of immunolabels into the remaining tissue–hydrogel matrix. Furthermore, the utility of tissue-

hydrogel hybridization and detergent perfusion extends beyond their capacity to facilitate rodent organ and whole-body clearing and immunolabeling [32,41]. For example, hydrogel embedding effectively stabilizes amorphous or fragile samples [41], such as sputum (unpublished results), for processing, and secures microorganisms to sites of infection. This latter property has proven valuable in studying bacterial colonization (personal communication with Dianne Newman). Although originally demonstrated in whole rodents, perfusion-based methods may also render large, excised samples such as primate and pig organs transparent via the recirculation of PARS reagents through catheterized organ vasculature [101], an undertaking which would be prohibitively slow via passive immersion-based clearing. Finally, after initial lipid extraction and/or solvation steps (Table 2, chemical clearing), most tissue-clearing protocols employ a refractive-index homogenization step to minimize differences in light deflection by the heterogeneous tissue biomolecules (Table 3, optical clearing). This is most commonly accomplished via immersing chemically cleared samples in a solution of matched refractive index, such as RIMS (Figure 2A) [32,41]; polyol and concentrated sugar or sugar alcohol solutions such as glycerol [22], sucrose and fructose [21,24,39,102]; or organic solvents such as BABB [27,28,82] and others (see Table 3).

The ability to expediently process and analyze samples without sectioning has revolutionized modern histology. For example, tissue clearing allows pathologists to map tumor cells in whole human biopsies and postmortem samples [41]. Likewise, the ability to conduct fast whole-body clearing, as granted by the perfusive force in the PARS methodology [39], opens new avenues for exploring small-molecule biodistribution, examining viral-vector tropism (Figure 1), and tracing peripheral nerve networks to their target organs (Table 1) [31,32,39,41]. For difficult-to-clear bone samples, PACT with decalcification (PACT-deCAL [41]), SeeDB [103], 3DISCO [28], Murray’s clear (1:2 Benzyl Alcohol: Benzyl Benzoate; BABB [27]) [104] and other decalcification methods [105] all facilitate mapping the three-dimensional architecture of skeletal tissue and stem cell niches [106]. Regardless of the clearing protocol used, all carry trade-offs in terms of the degree of optical transparency achieved, the maintenance of endogenous fluorescence, the preservation of cellular integrity, and the permeability of cleared tissue to macromolecule labels. Although clearing with organic solvents or with electrophoresis may deliver more rapid and effective clearing than passive methods involving immersion in aqueous solutions, these harsher methods may also hinder fluorescent imaging, prove incompatible with immunolabeling, or risk tissue damage (see Table 2). In selecting a specific protocol or shuffling aspects of multiple protocols [107], researchers must consider their project objectives (e.g., imaging sparse epitopes, whole-body tract tracing) and experimental constraints (e.g., integration with smFISH or electron microscopy studies on cleared samples). Thus, this comprehensive list of available protocols (Tables 2–3) will serve most experimental needs (Table 1).

Towards structure–function mapping with tissue clearing

For tissue-clearing methods to reach their full potential, several major challenges must first be tackled: (1) Imaging: large tissue volumes require specialized microscopy; (2) Data analysis: meaningful data must be extracted from terabyte data sets; (3) Access to functional information: markers of activity must be preserved during tissue processing.

Regarding the extraction of functional information, a record of neuronal activity can be encoded via transcriptional or biochemical changes. For example, immediate-early-gene activation (e.g. through *T*argeted *R*ecombination in *A*ctive *P*opulations, or TRAP [108–111]), Ca^{2+} influx, and voltage spikes can all be detected by genetically encoded fluorescing sensors (for reviews, see [112–114]) [53,111,115–118]. An exciting possibility for resolving neuronal activation across longer timescales is to pair this *in vivo* activity sensing with *ex vivo* analysis of previously active cell circuits using thick-tissue clearing. Specifically, genetically encoded stable fluorescent markers can permanently tag living cells that respond to time-restricted stimuli so that their chemical identity and connectivity can be probed post-mortem. One such marker, CaMPARI (calcium-modulated photoactivatable ratiometric integrator of neuronal activity), grants persistent quantitative detection of any neuronal activity that occurs during subsecond application of the photoconversion light [64,119]. One can envision the combined use of CaMPARI with subsequent tissue-clearing methods that preserve endogenous fluorescence (such as Sca*l*eS [40] clearing and RIMS incubation [32,41]) to map the activity of intact biological networks in response to behaviorally relevant stimuli.

As we learn more about the transcriptional correlates of neuronal activity, quantitative and multiplexed RNA detection in intact tissue could also serve the role of extracting functional proxies from deceased tissue. Combinatorial labeling (“barcoding”) via single-molecule fluorescence *in situ* hybridization (smFISH) [120,121] allows for simultaneous detection of mRNA transcripts for multiple genes within individual cells [122,123]. Importantly, smFISH has been validated in thick sections, wherein tissue clearing and swelling improve single-transcript resolution through reducing background and physically separating single-molecule labels [32,122]. Further enlargement of the optical space within a cell, either for fluorescently barcoding multiple transcripts or for examining single-cell morphology, may be achieved through recent protocols (e.g. ExM [72], ePACT [41]) that expand tissue four-fold or more with the possibility to retain endogenous fluorescence (Figure 2C–D for ePACT; [41]). Combined, these evolving technologies raise the possibility of single-cell transcriptomics with preserved spatial information. By applying high-resolution microscopy [58–60,124] to the detection of mRNA-binding probes (e.g., single-molecule hybridization chain reaction (smHCR) probes with high signal-to-noise [125–127]) in cleared and, if needed, expanded tissue, scientists will be able to achieve more robust single-molecule RNA detection and hence quantitative data for transcriptional profiling of intact circuits across organs [122,123,128].

Outlook

Studies in naturally transparent organisms have recently progressed to real-time monitoring of neuronal activity during controlled behavior via light-gated and light-emitting tools [118,129]. Although the protocols for tissue stabilization and lipid removal described above can produce samples with sufficient transparency for intact tissue imaging and rapid tissue phenotyping, these methods are limited to *ex vivo* use. Transparent or not, deceased tissue can offer only a static picture of neuronal connections. Even with a connectome in hand as a road-map for cellular networks, we would still be far from understanding the brain. For example, neuropeptides can act at a distance disregarding explicit wiring [130–132], parallel

pathways within a network can result in degeneracy in circuit function [133], and apparent structural connectivity (e.g. as elucidated via GRASP [134]) does not imply active synaptic connectivity [135]. A crucial next step will involve registering the three-dimensional information obtained through tissue-clearing with either *ex vivo* or *in vivo* cellular activity mapping. Compatible with cleared tissue imaging, methods such as TRAP [108–111] and smFISH [32,122] enable the permanent tagging of recently active cells in thick tissues. This snapshot only captures a single time point, however. What remains to be developed is a method for time-stamping signaling events across bulk cell populations such that the time-varying metabolic information from a single-cell's lifetime can be retrieved and cross-correlated to the metabolic records of all neighboring cells. To this end, single-cell transcriptomics [136,137] and 'molecular ticker tapes' (i.e. an engineered DNA polymerase mis-incorporates nucleotides into a DNA 'ticker tape' based on spikes in ion concentration [138,139]) represent two areas of promise.

A second approach under development aims to bring the CLARITY concept to living tissue. Namely, instead of altering tissue to reduce light-scattering, scientists are recruiting the power of ultrasound focusing at depth to deliver and collect light non-invasively from living tissue. Methods such as Time-Reversal Ultrasound-Encoded (TRUE) aim to correct the light-wavefront in scattering tissue [140] and currently enable focusing at depth within *ex vivo* tissue [141,142]. Because of its high sensitivity to motion, challenges remain in using TRUE for noninvasive deep-tissue imaging and light delivery *in vivo* [143]. One possibility is to combine advances in optical imaging, such as TRUE, with the application of gentle tissue clearing reagents *in vivo* to decrease autofluorescent background and homogenize the refractive index [144,145].

Bringing "clarity" to living tissue, when combined with developments in labeling, imaging, and computation, will enable mapping of anatomical and functional connectivity and will illuminate the workings of intact circuits with high temporal precision. Although whole-body imaging is still a nascent technology, analysis of the resulting volumetric datasets will convey a level of scientific understanding that cannot be replicated in a two-dimensional context; akin to previous work in the nematode and zebrafish, large-scale tissue clearing represents a first step towards a hermeneutic approach to mammalian biology.

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Box 1. Glossary of acronyms and terminology related to tissue-clearing and cell-mapping

3DISCO: Three-Dimensional Imaging of Solvent-Cleared Organs; 3DISCO and uDISCO versions.
AAV: Adeno-Associated Virus; multiple natural and non-natural serotypes, including AAV-PHP.B.
BABB: Benzyl Alcohol and Benzyl Benzoate; BABB and Murray's Clear techniques.
Brainbow: stochastic expression of multiple fluorescent proteins from a single transgene; Brainbow v1.0–3.2 in addition to other variants (e.g., Autobow, Flybow, Zebrabow, R26R–Confetti, MAGIC Marker).
CaMPARI: Calcium-Modulated PhotoActivatable Ratiometric Integrator of neuronal activity
CLARITY: Clear Lipid-exchanged Acrylamide-hybridized Rigid Imaging/immunostaining/*in situ* hybridization-compatible Tissue hYdrogel; CLARITY, advanced CLARITY, passive CLARITY, and stochastic-electrotransport versions.
CREATE: Cre-recombination-based AAV Targeted Evolution
CUBIC: Clear Unobstructed Brain Imaging cocktails and Computational analysis; CUBIC, advanced CUBIC and perfusion-CB variations.
Clear: a formamide-based optical clearing method; ClearT and ClearT2 (formamide/polyethylene glycol) variation.
DMSO: dimethyl sulfoxide
EDTA:ethylenediaminetetraacetic acid
ETC: Electrophoretic Tissue Clearing; clearing approach of CLARITY.
ePACT: expansion-PACT
ExM: Expansion Microscopy
Fruit: optical clearing method that utilizes an aqueous cocktail of fructose, urea, and α-thioglycerol.
GRASP: *GFP Reconstitution Across Synaptic Partners*
HCR: Hybridization Chain Reaction; operable with RNA and DNA probes
iDISCO: Immunolabeling-enabled 3D Imaging of Solvent-Cleared Organs; iDISCO and iDISCO+ variation.
IHC: Immunohistochemistry
NPS: Neuronal Positioning System
PACT: PAssive Clarity Technique
PACT-deCAL: PACT-deCALcification
PARS: Perfusion-assisted Agent Release *in Situ* ; PARS and PARS-CSF variation.
PFA: Paraformaldehyde
RI: refractive index
RIMS: Refractive Index Matching Solution; RIMS (histodenz-based) and sRIMS (sorbitol-based) variation.
Sca*l*e: a urea-based optical clearing method; Sca*l*eA2 and Sca*l*eU2 versions.
Sca*l*eS: a sorbitol-based optical clearing method; includes AbSca*l*e, Chemsca*l*e, and Sca*l*eSQ variations.
SDS: sodium dodecyl sulfate
SeeDB: See Deep Brain; SeeDB, SeeDB37 and SeeDB37ht variations.
smFISH: single-molecule Fluorescence *In Situ* Hybridization
Spalteholz's preparation: Benzyl benzoate and methyl salicylate
SWITCH: System-*W*de control of Interaction *T*ime and kinetics of CHemicals
TDE: 2,2'-thiodiethanol
Tissue-Hydrogel: tissue structure and/or molecular content may be stabilized via tissue-hydrogel crosslinking or embedding; multiple hydrogel

formulations, including any/all of acrylamide, bisacrylamide, paraformaldehyde, glutaraldehyde, sodium acrylate, agarose.
TRAP: *T*argeted *R*ecombination in *A*ctive *P*opulations
TRIO: ‘Tracing the Relationship between Input and Output’ method; TRIO and cTRIO methods.
TRUE: Time-Reversal Ultrasound-Encoded

Highlights

1. Tissue clearing and viral vectors for resolved 3D imaging of unsevered circuits
2. Size-adjustable tissue-hydrogels for sample stabilization and selective extraction
3. Whole-body clearing and labeling via *P*erfusion-assisted *A*gent *R*elease in *S*itu
4. High-throughput method for in vivo vector selection and bodywide transduction mapping
5. AVV vector for transgene expression brainwide via systemic injection in the adult

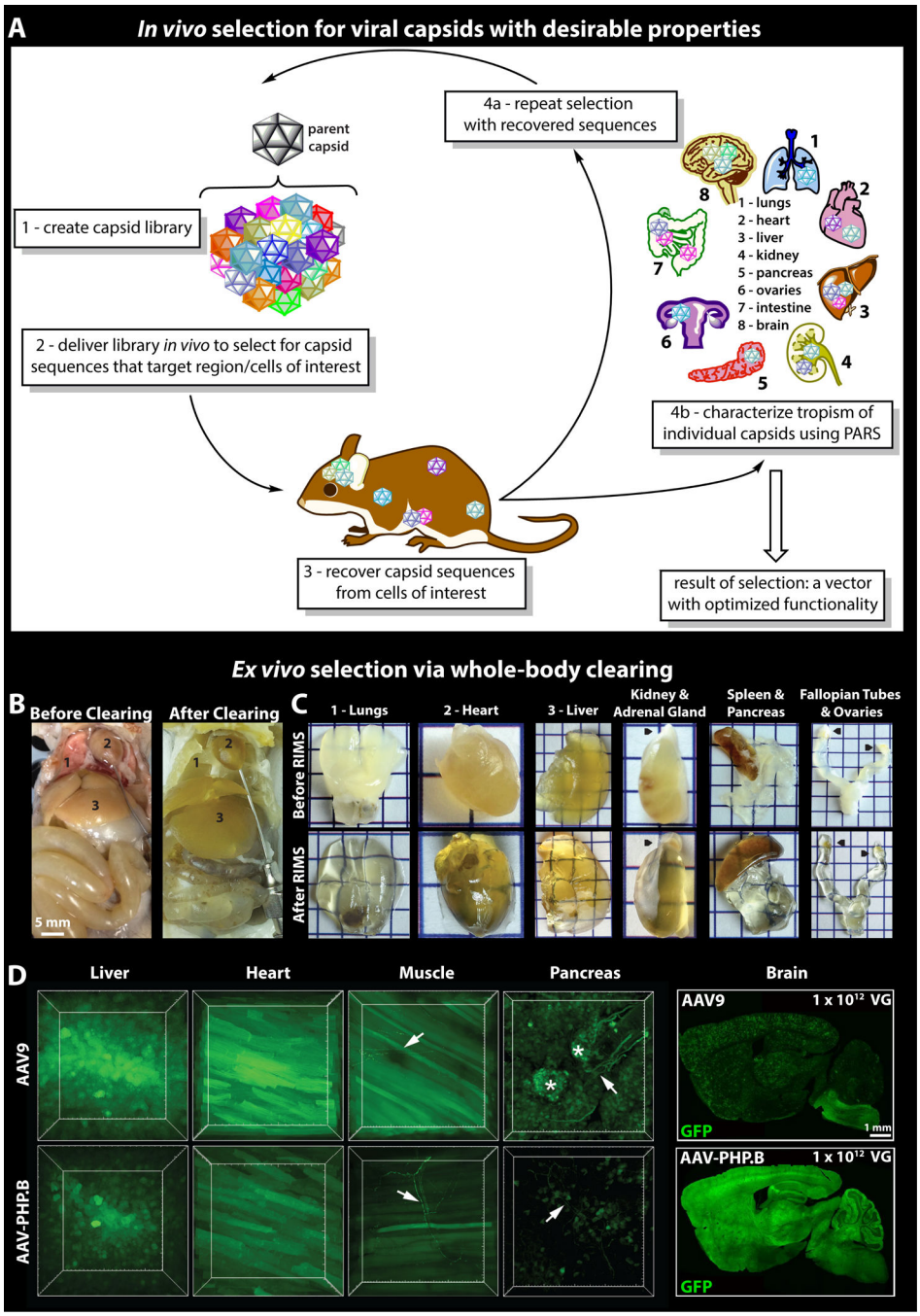

Figure 1.

Concept for an *in vivo* selection technology for panning large-scale libraries to identify compounds or biologicals with optimized physiological properties. Whole-body tissue clearing can then facilitate biodistribution mapping. For example, to engineer viral vectors for more effective transgene delivery, one strategy involves exposing live cells or whole-organisms to AAV capsid libraries and then identifying positive hits via a cell or tissue type-dependent recovery strategy (**A**). Whole-body clearing by Perfusion-Assisted Agent Release in Situ (PARS, [32,41]) speeds up the multi-organ assessment of vector variants expression

profiles. Internal organs before and after clearing (**B**). Individual PARS-cleared organs (**C**) before (top) or after (bottom) equilibration in RIMS, a Refractive Index Matching Solution [32,41], as imaging media. Black pointers correspond to the adrenal gland on the kidney, and to the ovaries on the fallopian tubes. Each square represents 0.5 cm^2. The qualitative assessment of cell-type transduction can be conducted by packaging fluorescent reporters in individual capsid variants and then simultaneously clearing all organs *in situ* (**D**). As proof-of-principle, a novel capsid variant (AAV-PHP.B, bottom), selected for enhanced brain transduction, was rapidly evolved from AAV9 (top). Comparisons of PARS-cleared organs demonstrate that AAV-PHP.B and AAV9 have similar cellular tropisms outside of the brain. Arrows (→) indicate neuronal morphology, and asterisks (*) designate pancreatic islets. Differences in brain transduction are depicted in the images of mouse brain sagittal sections. Figures 2A and 2D adapted from [53], and figures 2B–C adapted from [41].

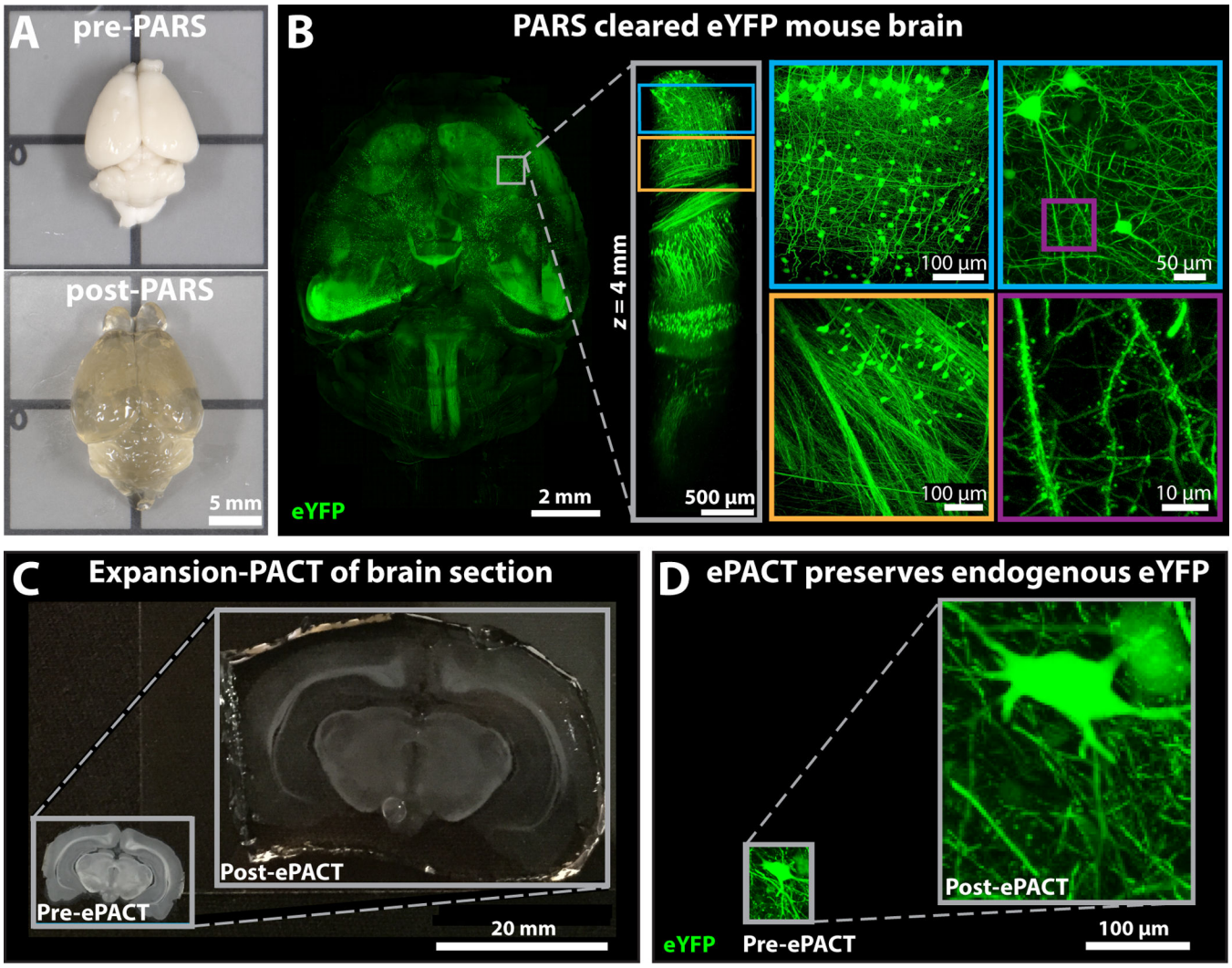

Figure 2.

Clearing techniques that enable high-resolution, volumetric imaging of tissue architecture and cellular morphology. Whole-body hydrogel embedding and detergent-based clearing via the PARS-CLARITY method [22,32,37,41] preserves gross tissue structure (**A**) and fine neuronal processes (**B**) alike, while the purposeful expansion of these tissue-hydrogel hybrids via water absorption (**C**) allows the visualization of subcellular detail via either native fluorescence (**D**), or probes for protein and nucleic acid detection [32]. ePACT permits the clearing and 4-fold expansion of 100 µm thick coronal brain sections with preservation of tissue shape, cellular morphology and native fluorescence. Figures 1A–B adapted from [32], and figures 1C–D adapted from [41].

Table 1

Anticipated Biomedical Applications of Modern Clearing Techniques

Application Areas	Cleared Tissue and Complementary Technologies
Assessing biodistribution of chemicals or biologicals; and screening compound libraries [53,91,146–152]	**Whole-body clearing[a] of rodents (embryos through aged adult; see Figure 1) Excised whole-organ delipidation through major blood vessels in larger mammalian subjects (e.g. pigs, non-human primates) [101,153] CREATE platform for viral vector screening in cleared samples (Fig. 1) [53]**
Labeling and imaging through dense, complex tissues [154–161] Mapping discrete cellular niches (e.g. stem cells, tumors) [162–168]	**PACT-deCAL [41], BABB [27,106] for bone Clearing tissue biopsies[b] and excised organs, or whole-body perfusion-clearing[a] in cancer models**
3D–tracing long-range fiber bundles (e.g. vagus nerve); lineage-mapping in neurodevelopment [169]	**Viral or transgenic labeling technologies (e.g. Brainbow [7], TRIO [6], Confetti [170], MAGIC markers [171]; Box 1) followed by whole-body clearing**
Monitoring the progression of cell death and tissue damage (e.g. stroke, infarcts), and the corresponding re-oxygenation [172,173]	**Whole-organ or whole-body clearing Perfusion labelling to counterstain intact vasculature and surrounding tissues**
Tracking nerve/axon regeneration and de/re-myelination; examining neuroplasticity at the synaptic level [28,115,174–180]	**Whole-body perfusion-clearing[a] and perfusion-labelling, and PACT-deCAL [41] to clear the vertebral column Co-registration of array tomography [181,182], light and electron microscopy datasets [8,73,161,183–187]**
Spectrally resolving subcellular labels (e.g. single molecule transcripts) within native tissue	**Multiplexed labelling and/or sequential barcoding with FISH [120–122] and HCR [127,128]; Neuronal positioning system (NPS) [8] Hydrogel-embedding and expansion-clearing (ExM [72], ePACT [41])**
Exploring topics in parasitology [188] and microbiology (e.g., biofilm formation, microbe distribution within a niche [189–192], host interaction with the microbiome [64,193])	**Hydrogel-embedding of fragile samples'[b], followed by gentle, passive whole-organ clearing to maintain bacterial colonization**
Extending the imaging depth range and resolution for optical coherence tomography [194–197] and photoacoustic tomography [141–143,145,198–205]	**Future prospects for optically clearing living tissue with optical and/or contrast clearing reagents (e.g. varying ratios of PEG-400, DMSO, and/or glycerol)**

[a]For whole-body clearing and perfusion-labeling methods, see [31,32,39,41], with detailed methods on PARS and perfusion-CUBIC in their respective *Nature Protocols*

[b]For further advice, see troubleshooting instructions at http://www.nature.com/nprot/journal/v10/n11/fig_tab/nprot.2015.122_T5.html [41]

Table 2

Methodological comparison and important considerations when choosing a tissue clearing protocol that achieves both macromolecular extraction and optical clarity.

Motivation	Method *Variations*	Sample Preparation[a]	Clearing Reagents[b]	Size Fluctuations	Fluorescence[c]	IHC[d]
Dehydration and Lipid Solvation						
To achieve transparency rapidly using organic solvents of high RI (precursors: Spalteholz [55], BABB [27])	**3DISCO [26,28,38,206]**	tetrahydrofuran dehydration	dichloromethane lipid solvation	shrinkage	YES (1–4d)	Limited
	iDISCO [36]	methanol dehydration or DMSO, PBS	dichloromethane	shrinkage	YES (1–4d)	YES
	uDISCO[e]	n/p[f]	n/p	shrinkage	YES	YES
Partial delipidation and hyperhydration						
To obtain a fluorescence-compatible solvent alternative via hyper-hydration of the delipidized sample	**Sca/eA2-U2 [23]**	n/a[f]	4 M urea, 10–30% glycerol hyperhydration	expansion	YES	NO
	Sca/eS (*AbSca/e, ChemSca/e Sca/eSQ*) [40]	n/a	2.7–9.1 M urea, 20–40% sorbitol, ≤5.0% Triton X-100, DMSO	NO	YES	YES
	CUBIC [25], *with decolorization* [35,39]	n/a	25% urea-50% sucrose aminoalcohol decolorization 15% Triton X-100 delipidation	expansion	YES	YES
Targeted biomolecule retention and rigorous delipidation						
To stabilize sample structure, macromolecular content, and fluorescent labeling using size adjustable, tissue-binding hydrogels	**CLARITY [22,37,62,110]**	tissue-hydrogel	4% SDS ETC delipidation [f]	reversible expansion	YES	YES
	CLARITY variations [29,30,110]		4% SDS ETC 4% SDS diffusion		YES	YES
	Stochastic Electrotransport [81]		4% SDS stochastic ETC		YES	YES
	PARS [32,41] *PACT* [32,41]	tissue-hydrogel	8% SDS perfusion 8% SDS diffusion	reversible expansion	YES	YES
	PACT-deCAL	tissue-hydrogel	8% SDS diffusion EDTA/EGTA decalcification	NO	YES	YES

Motivation	Method *Variations*	Sample Preparation[a]	Clearing Reagents[b]	Size Fluctuations	Fluorescence[c]	IHC[d]
	ExM [207] *ePACT* [41]	superabsorbent hydrogel	enzymatic digestion ±clearing	4–5x expansion	YES	YES
	SWITCH [208]	glutaraldehyde-tissue gel	200mM SDS diffusion, 60–80 °C	NO	NO	YES
Whole-body perfusion clearing						
To preserve body-brain connections and accelerate adult whole-organ preparation via clearing *in situ*	**PARS**	tissue-hydrogel	8% SDS perfusion clearing	minimal expansion	YES	YES-perfusion
	Perfusion CUBIC [39]	tissue-hydrogel	CUBIC reagent perfusion	n/d[f]	YES	Limited-perfusion
	Perfusion FRUIT [31]	n/a	FRUIT reagent perfusion	n/d	n/d	NO

[a] Sample preparation aside from standard fixation and brief post-fixation (e.g. transcardial perfusion with 4% PFA).

[b] Chemically/mechanically removing tissue macromolecular components (e.g. lipids, heme) to improve light probe penetration and reduce light scattering.

[c] Fluorescence preservation varies with fluorophore and user technique. A binary classification: YES = overall preservation of endogenous fluorescence, with any signal dimming mild; NO = major or complete endogenous fluorescence quenching due to reagent or procedural incompatibility with common fluorophores; if rapid signal decay, timeline for imaging in "( )". Also of note, moderate loss of fluorescence in CUBIC, PACT, and SeeDB tissues, and major quenching in 3DISCO tissues has been reported elsewhere [40].

[d] YES, NO: Compatible, incompatible with IHC and fluorescent labeling in thick samples and with multiple fluorophores; Limited: IHC possible with small-molecule stains and some antibodies, restrictions in immunofluorescence and/or deep antibody penetration; Perfusion-delivery of IHC reagents noted where applicable.

[e] Personal communication with Dr. Ali Ertürk on uDISCO, which allows preservation of endogenous fluorescence in fine processes for several weeks to months.

[f] abbreviations: n/p = not published, n/d = not determined, n/a = not applicable; see Box 1 for complete list.

Table 3

Sample mounting for enhanced optical clarity.

Method[a]	Sample Preparation	Clearing Reagents	Size Fluctuations	Fluorescence
organic solvents RI ~ 1.52–1.57	none	methyl salicylate [209]	shrinkage	NO
	Ultramicroscopy [27]	BABB	shrinkage	Y/N»
	3DISCO iDISCO	dibenzyl ether	shrinkage	Y/N
amides RI ~ 1.38–1.44	ClearT, ClearT2 [24]	formamide ± PEG	none, n/d[b]	Y/N
	Sca/eA2, Sca/eS, CUBIC, FRUIT	urea	slight -moderate expansion	YES
polyol and concentrated sugar or sugar alcohol solutions RI ~ 1.43–1.50, tunable	CLARITY, PACT, PARS	glycerol	slight expansion	YES
	SeeDB [21,102]	fructose	minimal	YES
	FRUIT	fructose + thioglycerol + urea	slight expansion	YES
	Sca/eA2	glycerol + urea	moderate expansion	YES
	CUBIC	sucrose + urea + triethanolamine	moderate expansion	YES
	Sca/eS, PARS, PACT	sorbitol, sRIMS	slight - moderate expansion	YES
aqueous contrast media RI ~ 1.46, tunable	CLARITY	Focus Clear: Diatrizoic acid	slight expansion	YES
	PACT, PARS, RIMS	RIMS: Histodenz	acute shrinkage, gradual expansion	YES
aqueous mounting media RI ~ 1.33–1.52, tunable	TDE [34]	2,2'-thiodiefhanol [83]	none	YES

[a] Optical clarity, or reduced light scattering through tissue, may be enhanced via homogenizing the refractive indices throughout heterogeneous tissues and at all material interfaces between the sample and objective lens

[b] Y/N = signal decay may necessitate prompt imaging upon sample mounting